



SEQUENCE LISTING

<110> Kevin Baker et al.

<120> HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR16

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<150> 09/637,856

<151> 2000-08-10

<150> 60/148,348

<151> 1999-08-12

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	130					135					140						
Gly	Phe	Ser	Asn	Ile	Ala	Thr	Phe	Met	Asp	Thr	Val	Val	Gly	Pro	Ser		
145					150					155					160		
Asp	Ser	Arg	Pro	Asp	Gly	Cys	Asn	Asn	Ser	Ser	Trp	Ile	Pro	Arg	Gly		
				165					170					175			
Asn	Tyr	Ile	Glu	Ser	Asn	Arg	Asp	Asp	Cys	Thr	Val	Ser	Leu	Ile	Tyr		
			180					185					190				
Ala	Val	His	Leu	Lys	Lys	Ser	Gly	Tyr	Val	Phe	Phe	Glu	Tyr	Gln	Tyr		
		195					200					205					
Val	Asp	Asn	Asn	Ile	Phe	Phe	Glu	Phe	Phe	Ile	Gln	Asn	Asp	Gln	Cys		
	210					215					220						
Gln	Glu	Met	Asp	Thr	Thr	Thr	Asp	Lys	Trp	Val	Lys	Leu	Thr	Asp	Asn		
225					230					235					240		
Gly	Glu	Trp	Gly	Ser	His	Ser	Val	Met	Leu	Lys	Ser	Gly	Thr	Asn	Ile		
				245					250					255			
Leu	Tyr	Trp	Arg	Thr	Thr	Gly	Ile	Leu	Met	Gly	Ser	Lys	Ala	Val	Lys		
			260					265					270				
Pro	Val	Leu	Val	Lys	Asn	Ile	Thr	Ile	Glu	Gly	Val	Ala	Tyr	Thr	Ser		
		275					280					285					
Glu	Cys	Phe	Pro	Cys	Lys	Pro	Gly	Thr	Phe	Ser	Asn	Lys	Pro	Gly	Ser		
	290					295					300						
Phe	Asn	Cys	Gln	Val	Cys	Pro	Arg	Asn	Thr	Tyr	Ser	Glu	Lys	Gly	Ala		
305					310					315					320		
Lys	Glu	Cys	Ile	Arg	Cys	Lys	Asp	Asp	Ser	Gln	Phe	Ser	Gly	Ser	Ser		
				325					330					335			
Glu	Cys	Thr	Glu	Arg	Pro	Pro	Cys	Thr	Thr	Lys	Asp	Tyr	Phe	Gln	Ile		
			340					345					350				
His	Thr	Pro	Cys	Asp	Glu	Glu	Gly	Lys	Thr	Gln	Ile	Met	Tyr	Lys	Trp		
		355					360					365					
Ile	Glu	Pro	Lys	Ile	Cys	Arg	Glu	Asp	Leu	Thr	Asp	Ala	Ile	Arg	Leu		
	370					375					380						

Pro	Pro	Ser	Gly	Glu	Lys	Lys	Asp	Cys	Pro	Pro	Cys	Asn	Pro	Gly	Phe	385	390	395	400
Tyr	Asn	Asn	Gly	Ser	Ser	Ser	Cys	His	Pro	Cys	Pro	Pro	Gly	Thr	Phe	405	410		415
Ser	Asp	Gly	Thr	Lys	Glu	Cys	Arg	Pro	Cys	Pro	Ala	Gly	Thr	Glu	Pro	420	425		430
Ala	Leu	Gly	Phe	Glu	Tyr	Lys	Trp	Trp	Asn	Val	Leu	Pro	Gly	Asn	Met	435	440		445
Lys	Thr	Ser	Cys	Phe	Asn	Val	Gly	Asn	Ser	Lys	Cys	Asp	Gly	Met	Asn	450	455		460
Gly	Trp	Glu	Val	Ala	Gly	Asp	His	Ile	Gln	Ser	Gly	Ala	Gly	Gly	Ser	465	470		475
Asp	Asn	Asp	Tyr	Leu	Ile	Leu	Asn	Leu	His	Ile	Pro	Gly	Phe	Lys	Pro	485	490		495
Pro	Thr	Ser	Met	Thr	Gly	Ala	Thr	Gly	Ser	Glu	Leu	Gly	Arg	Ile	Thr	500	505		510
Phe	Val	Phe	Glu	Thr	Leu	Cys	Ser	Ala	Asp	Cys	Val	Leu	Tyr	Phe	Met	515	520		525
Val	Asp	Ile	Asn	Arg	Lys	Ser	Thr	Asn	Val	Val	Glu	Ser	Trp	Gly	Gly	530	535		540
Thr	Lys	Glu	Lys	Gln	Ala	Tyr	Thr	His	Ile	Ile	Phe	Lys	Asn	Ala	Thr	545	550		555
Phe	Thr	Phe	Thr	Trp	Ala	Phe	Gln	Arg	Thr	Asn	Gln	Gly	Gln	Asp	Asn	565	570		575
Arg	Arg	Phe	Ile	Asn	Asp	Met	Val	Lys	Ile	Tyr	Ser	Ile	Thr	Ala	Thr	580	585		590
Asn	Ala	Val	Asp	Gly	Val	Ala	Ser	Ser	Cys	Arg	Ala	Cys	Ala	Leu	Gly	595	600		605
Ser	Glu	Gln	Ser	Gly	Ser	Ser	Cys	Val	Pro	Cys	Pro	Pro	Gly	His	Tyr	610	615		620
Ile	Glu	Lys	Glu	Thr	Asn	Gln	Cys	Lys	Glu	Cys	Pro	Pro	Asp	Thr	Tyr	625	630		635
																			640

Leu Ser Ile His Gln Val Tyr Gly Lys Glu Ala Cys Ile Pro Cys Gly
 645 650 655
 Pro Gly Ser Lys Asn Asn Gln Asp His Ser Val Cys Tyr Ser Asp Cys
 660 665 670
 Phe Phe Tyr His Glu Lys Glu Asn Gln Ile Leu His Tyr Asp Phe Ser
 675 680 685
 Asn Leu Ser Ser Val Gly Ser Leu Met Asn Gly Pro Ser Phe Thr Ser
 690 695 700
 Lys Gly Thr Lys Tyr Phe His Phe Phe Asn Ile Ser Leu Cys Gly His
 705 710 715 720
 Glu Gly Lys Lys Met Ala Leu Cys Thr Asn Asn Ile Thr Asp Phe Thr
 725 730 735
 Val Lys Glu Ile Val Ala Gly Ser Asp Asp Tyr Thr Asn Leu Val Gly
 740 745 750
 Ala Phe Val Cys Gln Ser Thr Ile Ile Pro Ser Glu Ser Lys Gly Phe
 755 760 765
 Arg Ala Ala Leu Ser Ser Gln Ser Ile Ile Leu Ala Asp Thr Phe Ile
 770 775 780
 Gly Val Thr Val Glu Thr Thr Leu Lys Asn Ile Asn Ile Lys Glu Asp
 785 790 795 800
 Met Phe Pro Val Pro Thr Ser Gln Ile Pro Asp Val His Phe Phe Tyr
 805 810 815
 Lys Ser Ser Thr Ala Thr Thr Ser Cys Ile Asn Gly Arg Ser Thr Ala
 820 825 830
 Val Lys Met Arg Cys Asn Pro Thr Lys Ser Gly Ala Gly Val Ile Ser
 835 840 845
 Val Pro Ser Lys Cys Pro Ala Gly Thr Cys Asp Gly Cys Thr Phe Tyr
 850 855 860
 Phe Leu Trp Glu Ser Ala Glu Ala Cys Pro Leu Cys Thr Glu His Asp
 865 870 875 880
 Phe His Glu Ile Glu Gly Ala Cys Lys Arg Gly Phe Gln Glu Thr Leu
 885 890 895

Tyr Val Trp Asn Glu Pro Lys Trp Cys Ile Lys Gly Ile Ser Leu Pro
 900 905 910
 Glu Lys Lys Leu Ala Thr Cys Glu Thr Val Asp Phe Trp Leu Lys Val
 915 920 925
 Gly Ala Gly Val Gly Ala Phe Thr Ala Val Leu Leu Val Ala Leu Thr
 930 935 940
 Cys Tyr Phe Trp Lys Lys Asn Gln Lys Leu Glu Tyr Lys Tyr Ser Lys
 945 950 955 960
 Leu Val Met Thr Thr Asn Ser Lys Glu Cys Glu Leu Pro Ala Ala Asp
 965 970 975
 Ser Cys Ala Ile Met Glu Gly Glu Asp Asn Glu Glu Glu Val Val Tyr
 980 985 990
 Ser Asn Lys Gln Ser Leu Leu Gly Lys Leu Lys Ser Leu Ala Thr Lys
 995 1000 1005
 Glu Lys Glu Asp His Phe Glu Ser Val Gln Leu Lys Thr Ser Arg
 1010 1015 1020
 Ser Pro Asn Ile
 1025
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 1 5 10 15
 Thr Leu Ala Thr Ala Asp Ile Pro Thr Ser Ser Leu Pro His Ala Pro
 20 25 30
 Val Asn Gly Ala Cys Asp Glu Gly Glu Tyr Leu Asp Lys Arg His Asn
 35 40 45
 Gln Cys Cys Asn Gln Cys Pro Pro Gly Glu Phe Ala Lys Val Arg Cys
 50 55 60
 Asn Gly Asn Asp Asn Thr Lys Cys Glu Arg Cys Pro Pro His Thr Tyr

65		70		75		80									
Thr	Ala	Ile	Pro	Asn	Tyr	Ser	Asn	Gly	Cys	His	Gln	Cys	Arg	Lys	Cys
				85					90					95	
Pro	Thr	Gly	Ser	Phe	Asp	Lys	Val	Lys	Cys	Thr	Gly	Thr	Gln	Asn	Ser
			100					105					110		
Lys	Cys	Ser	Cys	Leu	Pro	Gly	Trp	Tyr	Cys	Ala	Thr	Asp	Ser	Ser	Gln
		115					120					125			
Thr	Glu	Asp	Cys	Arg	Asp	Cys	Ile	Pro	Lys	Arg	Arg	Cys	Pro	Cys	Gly
	130					135					140				
Tyr	Phe	Gly	Gly	Ile	Asp	Glu	Gln	Gly	Asn	Pro	Ile	Cys	Lys	Ser	Cys
145					150					155					160
Cys	Val	Gly	Glu	Tyr	Cys	Asp	Tyr	Leu	Arg	Asn	Tyr	Arg	Leu	Asp	Pro
				165					170					175	
Phe	Pro	Pro	Cys	Lys	Leu	Ser	Lys	Cys	Asn						
			180					185							

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<400> 6

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Leu	Leu	Leu	Gly	Leu	Gly	Leu	Ser	Thr	Val	Thr	Gly	Leu	His	Cys	Val
			20					25					30		
Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	Cys	His	Glu	Cys	Arg	Pro
		35					40					45			
Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	Ser	Gln	Asn	Thr	Val	Cys
	50					55					60				
Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	Val	Val	Ser	Ser	Lys	Pro
65					70				75					80	
Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	Ser	Gly	Ser	Glu	Arg	Lys
				85					90					95	

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
100 105 110

Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys
115 120 125

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
130 135 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn
145 150 155 160

Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
165 170 175

Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr
180 185 190

Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu
195 200 205

Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
210 215 220

Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
225 230 235 240

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
245 250 255

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
260 265 270

Thr Leu Ala Lys Ile
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Pro Cys Gln Glu Lys Asp Tyr His
1 5

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Gly Lys Glu Cys Thr Phe Ser Cys
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Gly Cys Asn Asn Ser Ser Trp Ile
1 5

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Phe Glu Phe Phe Ile Gln Asn Asp
1 5

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Ser Gln Phe Ser Gly Ser Ser Glu
1 5

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Glu Glu Gly Lys Thr Gln Ile Met
1 5

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Asp Gly Thr Lys Glu Cys Arg Pro
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Pro Gly Phe Lys Pro Pro Thr Ser

1 5

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Tyr Phe Met Val Asp Ile Asn Arg
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Gln Cys Gln Asp Asn Arg Arg Phe
1 5

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Lys Asn Asn Gln Asp His Ser Val
1 5

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Cys Gly His Glu Gly Lys Lys Met
1 5

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Asp Thr Phe Ile Gly Val Thr Val
1 5

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Phe Phe Tyr Lys Ser Ser Thr Ala
1 5

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Ile Ser Val Pro Ser Lys Cys Pro
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Arg Gly Phe Gln Glu Thr Leu Tyr
1 5

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Lys Asn Gln Lys Lys Lys Lys Thr
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Lys Asn Gln Lys Leu Glu Tyr Lys
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Leu Ala Thr Lys Glu Lys Glu Asp
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Arg Leu His Gly Ser Gly His Ser Arg Leu Ala Ala Ala Ile Ser
20 25 30

Ile Ala Leu Lys Ala Phe Ser Cys Ala Ser Gly
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Cys Thr Glu Arg Pro Pro Cys Thr Thr Lys Asp Tyr Phe Gln Ile His
1 5 10 15

Thr Pro Cys Asp Glu Glu Gly Lys Thr Gln Ile Met Tyr Lys Trp Ile
20 25 30

Glu Pro Lys Ile Cys Arg Glu Asp Leu Thr Asp Ala Ile Arg Leu Pro
35 40 45

Pro Ser Gly Glu Lys Lys Asp Cys Pro Pro Cys Asn Pro Gly Phe Tyr
50 55 60

Asn Asn Gly Ser Ser Ser Cys His Pro Cys
65 70

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<211> 29
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Thr Lys Gly Trp Trp Ile Ile Ser Gly Ser Ser Ser Leu Arg Arg Thr
1 5 10 15

Phe Lys His Ala Phe Cys Ser Thr Phe Ala Ala Glu Cys
20 25

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<400> 33

Phe Lys Met Asp Gly Ile Ile Tyr Ser Lys Arg Phe Lys His Ile Thr
1 5 10 15

Ile Val Met Trp Thr Gln Cys Leu Gln Arg Val Trp Thr Gly Met Ile
20 25 30

Lys Pro Pro
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<211> 37
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Gln Asp Asn Arg Pro Ile Pro Pro Leu Ser Ile Ser Ile Val Pro Tyr
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 Val Ser Ile Val Ala Gly Leu Ile Leu Trp Ile Ser Ile Asp Val Thr
 20 25 30
 Phe Pro Arg Arg Phe
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 20 25 30
 Glu Gly Glu Asp Asn Glu Glu Glu Val Val Tyr Ser Asn Lys Gln Ser
 35 40 45
 Leu Leu Gly Lys Leu Lys Ser Leu Ala Thr Lys Glu Lys Glu Asp His
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 Phe Glu Ser Val Gln Leu Lys Thr Ser Arg Ser Pro Asn Ile
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<210> 40

<211> 27

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27

<210> 41

<211> 59

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<400> 41

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120
tctcccggac tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg
180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg
240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact
300
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg
360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc
420
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct
480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga
540
ccacgcctcc cgtgctggac tccgacggct ccttcttctct ctacagcaag ctcaccgtgg
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acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc
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733

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<213> human

<400> 43

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Gly Ser Gly Ile Lys Phe Asp Glu Trp Asp Glu Leu Pro Ala Gly Phe
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Ser Asn Ile Ala Thr Phe Met Asp Thr Val Val Gly Pro Ser Asp Ser
35        40        45
Arg Pro Asp Gly Cys Asn Asn Ser Ser Trp Ile Pro Arg Gly Asn Tyr
50        55        60
Ile Glu Ser Asn Arg Asp Asp Cys Thr Val Ser Leu Ile Tyr Ala Val
65        70        75        80
His Leu Lys Lys Ser Gly Tyr Val Phe Phe Glu Tyr Gln Tyr Val Asp
85        90        95
Asn Asn Ile Phe Phe Glu Phe Phe Ile Gln Asn Asp Gln Cys Gln Glu
100       105       110
Met Asp Thr Thr Thr Asp Lys Trp Val Lys Leu Thr Asp Asn Gly Glu
115       120       125
Trp Gly Ser His Ser Val Met Leu Lys Ser Gly Thr Asn Ile Leu Tyr
130       135       140
Trp Arg Thr Thr Gly Ile Leu Met Gly Ser Lys Ala Val Lys Pro Val
145       150       155       160
Leu Val Lys Asn Ile Thr Ile Glu Gly Val Ala Tyr Thr Ser Glu Cys
165       170       175
Phe Pro Cys Lys Pro Gly Thr Phe Ser Asn Lys Pro Gly Ser Phe Asn
180       185       190
Cys Gln Val Cys Pro Arg Asn Thr Tyr Ser Glu Lys Gly Ala Lys Glu
195       200       205
Cys Ile Arg Cys Lys Asp Asp Ser Gln Phe Ser Glu Glu Gly Ser Ser
210       215       220
Glu Cys Thr Glu Arg Pro Pro Cys Thr Thr Lys Asp Tyr Phe Gln Ile
225       230       235       240

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His	Thr	Pro	Cys	Asp	Glu	Glu	Gly	Lys	Thr	Gln	Ile	Met	Tyr	Lys	Trp
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Ile	Glu	Pro	Lys	Ile	Cys	Arg	Glu	Asp	Leu	Thr	Asp	Ala	Ile	Arg	Leu
			260					265					270		
Pro	Pro	Ser	Gly	Glu	Lys	Lys	Asp	Cys	Pro	Pro	Cys	Asn	Pro	Gly	Phe
		275					280					285			
Tyr	Asn	Asn	Gly	Ser	Ser	Ser	Cys	His	Pro	Cys	Pro	Pro	Gly	Thr	Phe
	290					295					300				
Ser	Asp	Gly	Thr	Lys	Glu	Cys	Arg	Pro	Cys	Pro	Ala	Gly	Thr	Glu	Pro
305					310					315					320
Ala	Leu	Gly	Phe	Glu	Tyr	Lys	Trp	Trp	Asn	Val	Leu	Pro	Gly	Asn	Met
				325					330					335	
Lys	Thr	Ser	Cys	Phe	Asn	Val	Gly	Asn	Ser	Lys	Cys	Asp	Gly	Met	Asn
			340					345					350		
Gly	Trp	Glu	Val	Ala	Gly	Asp	His	Ile	Gln	Ser	Gly	Ala	Gly	Gly	Ser
		355					360					365			
Asp	Asn	Asp	Tyr	Leu	Ile	Leu	Asn	Leu	His	Ile	Pro	Gly	Phe	Lys	Pro
	370					375					380				
Pro	Thr	Ser	Met	Thr	Gly	Ala	Thr	Gly	Ser	Glu	Leu	Gly	Arg	Ile	Thr
385					390					395					400
Phe	Val	Phe	Glu	Thr	Leu	Cys	Ser	Ala	Asp	Cys	Val	Leu	Tyr	Phe	Met
				405					410					415	
Val	Asp	Ile	Asn	Arg	Lys	Ser	Thr	Asn	Val	Val	Glu	Ser	Trp	Gly	Gly
			420					425					430		
Thr	Lys	Glu	Lys	Gln	Ala	Tyr	Thr	His	Ile	Ile	Phe	Lys	Asn	Ala	Thr
		435					440					445			
Phe	Thr	Phe	Thr	Trp	Gly	Ile	Pro	Arg	Glu	Leu	Ile	Gln	Gly	Pro	Arg
	450					455					460				